

GenCore version 5.1.6
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Om nucleic - nucleic search, using sw model

Run on: October 25, 2005, 05:40:18 ; Search time 3651 Seconds
 (without alignments)
 14222.654 Million cell updates/sec

Title: US-10-077-111-12

Perfect score: 1272

Sequence: 1. gaatttcggcttccacctgccc.....acaccaaaatggaaatcc 1272

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending patents NA Main: *

1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq: *
 2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq: *
 3: /cgn2_6/ptodata/1/pna/PCTUS3_COMB.seq: *
 4: /cgn2_6/ptodata/1/pna/US06_COMB.seq: *
 5: /cgn2_6/ptodata/1/pna/US07_COMB.seq: *
 6: /cgn2_6/ptodata/1/pna/US08_COMB.seq: *
 7: /cgn2_6/ptodata/1/pna/US09_COMB.seq: *
 8: /cgn2_6/ptodata/1/pna/US082_COMB.seq: *
 9: /cgn2_6/ptodata/1/pna/US093_COMB.seq: *
 10: /cgn2_6/ptodata/1/pna/US094_COMB.seq: *
 11: /cgn2_6/ptodata/1/pna/US085_COMB.seq: *
 12: /cgn2_6/ptodata/1/pna/US086_COMB.seq: *
 13: /cgn2_6/ptodata/1/pna/US087_COMB.seq: *
 14: /cgn2_6/ptodata/1/pna/US088_COMB.seq: *
 15: /cgn2_6/ptodata/1/pna/US089_COMB.seq: *
 16: /cgn2_6/ptodata/1/pna/US090_COMB.seq: *
 17: /cgn2_6/ptodata/1/pna/US091_COMB.seq: *
 18: /cgn2_6/ptodata/1/pna/US092_COMB.seq: *
 19: /cgn2_6/ptodata/1/pna/US092B_COMB.seq: *
 20: /cgn2_6/ptodata/1/pna/US093A_COMB.seq: *
 21: /cgn2_6/ptodata/1/pna/US093B_COMB.seq: *
 22: /cgn2_6/ptodata/1/pna/US094_COMB.seq: *
 23: /cgn2_6/ptodata/1/pna/US095A_COMB.seq: *
 24: /cgn2_6/ptodata/1/pna/US095B_COMB.seq: *
 25: /cgn2_6/ptodata/1/pna/US095C_COMB.seq: *
 26: /cgn2_6/ptodata/1/pna/US095D_COMB.seq: *
 27: /cgn2_6/ptodata/1/pna/US096A_COMB.seq: *
 28: /cgn2_6/ptodata/1/pna/US096B_COMB.seq: *
 29: /cgn2_6/ptodata/1/pna/US096C_COMB.seq: *
 30: /cgn2_6/ptodata/1/pna/US096D_COMB.seq: *
 31: /cgn2_6/ptodata/1/pna/US096E_COMB.seq: *
 32: /cgn2_6/ptodata/1/pna/US097A_COMB.seq: *
 33: /cgn2_6/ptodata/1/pna/US097B_COMB.seq: *
 34: /cgn2_6/ptodata/1/pna/US097C_COMB.seq: *
 35: /cgn2_6/ptodata/1/pna/US097D_COMB.seq: *
 36: /cgn2_6/ptodata/1/pna/US098A_COMB.seq: *
 37: /cgn2_6/ptodata/1/pna/US098C_COMB.seq: *
 38: /cgn2_6/ptodata/1/pna/US098D_COMB.seq: *
 39: /cgn2_6/ptodata/1/pna/US099A_COMB.seq: *
 40: /cgn2_6/ptodata/1/pna/US099B_COMB.seq: *
 41: /cgn2_6/ptodata/1/pna/US099C_COMB.seq: *
 42: /cgn2_6/ptodata/1/pna/US099D_COMB.seq: *
 43: /cgn2_6/ptodata/1/pna/US099E_COMB.seq: *

44: /cgn2_6/ptodata/1/pna/US09F_COMB.seq: *
 45: /cgn2_6/ptodata/1/pna/US100G_COMB.seq: *
 46: /cgn2_6/ptodata/1/pna/US100A_COMB.seq: *
 47: /cgn2_6/ptodata/1/pna/US100B_COMB.seq: *
 48: /cgn2_6/ptodata/1/pna/US101A_COMB.seq: *
 49: /cgn2_6/ptodata/1/pna/US101B_COMB.seq: *
 50: /cgn2_6/ptodata/1/pna/US102A_COMB.seq: *
 51: /cgn2_6/ptodata/1/pna/US102B_COMB.seq: *
 52: /cgn2_6/ptodata/1/pna/US103A_COMB.seq: *
 53: /cgn2_6/ptodata/1/pna/US103B_COMB.seq: *
 54: /cgn2_6/ptodata/1/pna/US104A_COMB.seq: *
 55: /cgn2_6/ptodata/1/pna/US104B_COMB.seq: *
 56: /cgn2_6/ptodata/1/pna/US105A_COMB.seq: *
 57: /cgn2_6/ptodata/1/pna/US106A_COMB.seq: *
 58: /cgn2_6/ptodata/1/pna/US107A_COMB.seq: *
 59: /cgn2_6/ptodata/1/pna/US107B_COMB.seq: *
 60: /cgn2_6/ptodata/1/pna/US108A_COMB.seq: *
 61: /cgn2_6/ptodata/1/pna/US109A_COMB.seq: *
 62: /cgn2_6/ptodata/1/pna/US109B_COMB.seq: *
 63: /cgn2_6/ptodata/1/pna/US109C_COMB.seq: *
 64: /cgn2_6/ptodata/1/pna/US109D_COMB.seq: *
 65: /cgn2_6/ptodata/1/pna/US109E_COMB.seq: *
 66: /cgn2_6/ptodata/1/pna/US109F_COMB.seq: *
 67: /cgn2_6/ptodata/1/pna/US109G_COMB.seq: *
 68: /cgn2_6/ptodata/1/pna/US110_COMB.seq: *
 69: /cgn2_6/ptodata/1/pna/US100_COMB.seq: *
 70: /cgn2_6/ptodata/1/pna/US001_COMB.seq: *
 71: /cgn2_6/ptodata/1/pna/US002_COMB.seq: *
 72: /cgn2_6/ptodata/1/pna/US003_COMB.seq: *
 73: /cgn2_6/ptodata/1/pna/US004_COMB.seq: *
 74: /cgn2_6/ptodata/1/pna/US005_COMB.seq: *
 75: /cgn2_6/ptodata/1/pna/US006_COMB.seq: *
 76: /cgn2_6/ptodata/1/pna/US007_COMB.seq: *
 77: /cgn2_6/ptodata/1/pna/US008_COMB.seq: *
 78: /cgn2_6/ptodata/1/pna/US009_COMB.seq: *
 79: /cgn2_6/ptodata/1/pna/US010_COMB.seq: *
 80: /cgn2_6/ptodata/1/pna/US011_COMB.seq: *
 81: /cgn2_6/ptodata/1/pna/US012_COMB.seq: *
 82: /cgn2_6/ptodata/1/pna/US013_COMB.seq: *
 83: /cgn2_6/ptodata/1/pna/US014_COMB.seq: *
 84: /cgn2_6/ptodata/1/pna/US015_COMB.seq: *
 85: /cgn2_6/ptodata/1/pna/US016_COMB.seq: *
 86: /cgn2_6/ptodata/1/pna/US017_COMB.seq: *
 87: /cgn2_6/ptodata/1/pna/US018_COMB.seq: *
 88: /cgn2_6/ptodata/1/pna/US019_COMB.seq: *
 89: /cgn2_6/ptodata/1/pna/US020_COMB.seq: *
 90: /cgn2_6/ptodata/1/pna/US021_COMB.seq: *
 91: /cgn2_6/ptodata/1/pna/US022_COMB.seq: *
 92: /cgn2_6/ptodata/1/pna/US023A_COMB.seq: *
 93: /cgn2_6/ptodata/1/pna/US023B_COMB.seq: *
 94: /cgn2_6/ptodata/1/pna/US024_COMB.seq: *
 95: /cgn2_6/ptodata/1/pna/US025_COMB.seq: *
 96: /cgn2_6/ptodata/1/pna/US026_COMB.seq: *
 97: /cgn2_6/ptodata/1/pna/US027_COMB.seq: *
 98: /cgn2_6/ptodata/1/pna/US028_COMB.seq: *
 99: /cgn2_6/ptodata/1/pna/US029_COMB.seq: *
 100: /cgn2_6/ptodata/1/pna/US030_COMB.seq: *
 101: /cgn2_6/ptodata/1/pna/US031_COMB.seq: *
 102: /cgn2_6/ptodata/1/pna/US032_COMB.seq: *
 103: /cgn2_6/ptodata/1/pna/US033_COMB.seq: *
 104: /cgn2_6/ptodata/1/pna/US034_COMB.seq: *
 105: /cgn2_6/ptodata/1/pna/US035_COMB.seq: *
 106: /cgn2_6/ptodata/1/pna/US036_COMB.seq: *
 107: /cgn2_6/ptodata/1/pna/US037_COMB.seq: *
 108: /cgn2_6/ptodata/1/pna/US038_COMB.seq: *
 109: /cgn2_6/ptodata/1/pna/US039_COMB.seq: *
 110: /cgn2_6/ptodata/1/pna/US040_COMB.seq: *
 111: /cgn2_6/ptodata/1/pna/US041_COMB.seq: *
 112: /cgn2_6/ptodata/1/pna/US042_COMB.seq: *
 113: /cgn2_6/ptodata/1/pna/US043_COMB.seq: *
 114: /cgn2_6/ptodata/1/pna/US044_COMB.seq: *
 115: /cgn2_6/ptodata/1/pna/US045_COMB.seq: *
 116: /cgn2_6/ptodata/1/pna/US046_COMB.seq: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
------------	-------------	--------	-------	-------------

Run on: October 25, 2005, 02:16:03 ; Search time 1341 Seconds
(without alignments)
4061.146 Million cell updates/sec

Title: US-10-077-111-13
Perfect score: 2047
Sequence: 1 MVKULIHTLADHGDDVNCCAF.....LTPNRTLKMAINRMLETHOK 384

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 26938570 seqs, 7091142127 residues
Total number of hits satisfying chosen parameters: 53877140

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+P2n.model -DEV=x1h
-Q=/cgn2.1/USPRO.spool/US10077111/runmat 24102005_072847 8258/app_query.fasta_1.583
-DB=Pending_Patents_NA_New -NEW_COMB_SEQ:
-LOOPEXT=0 -UNITS=bit -START=1 -END=1 -MATRIX=blosum62 -MINMATCH=0.1 -LOOPCL=0
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=PTO -HRAPSIZE=500 -MINLEN=200000000
-USER=US10077111@cgn1.1-141@runat 24102005_072847 8258 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMBOD=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPBXT=0.5 -FGAPOP=6
-FGAPBXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

```

1: /cgn2.6/ptodata/1/pna/PCT_NEW_COMB_SEQ:*
2: /cgn2.6/ptodata/1/pna/PCT_NEW_COMB_SEQ:*
3: /cgn2.6/ptodata/1/pna/US06_NEW_COMB_SEQ:*
4: /cgn2.6/ptodata/1/pna/US07_NEW_COMB_SEQ:*
5: /cgn2.6/ptodata/1/pna/US08_NEW_COMB_SEQ:*
6: /cgn2.6/ptodata/1/pna/US09_NEW_COMB_SEQ:*
7: /cgn2.6/ptodata/1/pna/US09_NEW_COMB_SEQ:*
8: /cgn2.6/ptodata/1/pna/US09_NEW_COMB_SEQ:*
9: /cgn2.6/ptodata/1/pna/US10_NEW_COMB_SEQ:*
10: /cgn2.6/ptodata/1/pna/US10_NEW_COMB_SEQ:*
11: /cgn2.6/ptodata/1/pna/US10_NEW_COMB_SEQ:*
12: /cgn2.6/ptodata/1/pna/US10_NEW_COMB_SEQ:*
13: /cgn2.6/ptodata/1/pna/US10_NEW_COMB_SEQ:*
14: /cgn2.6/ptodata/1/pna/US10_NEW_COMB_SEQ:*
15: /cgn2.6/ptodata/1/pna/US10_NEW_COMB_SEQ:*
16: /cgn2.6/ptodata/1/pna/US10_NEW_COMB_SEQ:*
17: /cgn2.6/ptodata/1/pna/US10_NEW_COMB_SEQ:*
18: /cgn2.6/ptodata/1/pna/US10_NEW_COMB_SEQ:*
19: /cgn2.6/ptodata/1/pna/US10_NEW_COMB_SEQ:*
20: /cgn2.6/ptodata/1/pna/US11_NEW_COMB_SEQ:*
21: /cgn2.6/ptodata/1/pna/US11_NEW_COMB_SEQ:*
22: /cgn2.6/ptodata/1/pna/US11_NEW_COMB_SEQ:*
23: /cgn2.6/ptodata/1/pna/US11_NEW_COMB_SEQ:*
24: /cgn2.6/ptodata/1/pna/US11_NEW_COMB_SEQ:*
25: /cgn2.6/ptodata/1/pna/US11_NEW_COMB_SEQ:*
26: /cgn2.6/ptodata/1/pna/US11_NEW_COMB_SEQ:*
27: /cgn2.6/ptodata/1/pna/US60_NEW_COMB_SEQ:*
```

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OM nucleic - nucleic search, using sw model

Run on: October 25, 2005, 05:49:01 ; Search time 5929 Seconds
(without alignments)
3067.275 Million cell updates/sec

Title: US-10-077-111-12

Perfect score: 1272
Sequence: 1 gaattccggcttccacctggg.....acacccaaaggtaaaatcc 1272

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27700967 seqs, 7148314824 residues

Total number of hits satisfying chosen parameters: 55401934

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

```

Pending Patents NA New:*
1: /cgn2_6/ptodata/7/pna/PCT_NEW_COMB_seq:*
2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB_seq2:*
3: /cgn2_6/ptodata/2/pna/US05_NEW_COMB_seq:*
4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB_seq:*
5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB_seq:*
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB_seq:*
7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB_seq1:*
8: /cgn2_6/ptodata/2/pna/US09_NEW_COMB_seq2:*
9: /cgn2_6/ptodata/2/pna/US10_NEW_COMB_seq:*
10: /cgn2_6/ptodata/2/pna/US10_NEW_COMB_seq0:*
11: /cgn2_6/ptodata/2/pna/US10_NEW_COMB_seq1:*
12: /cgn2_6/ptodata/2/pna/US10_NEW_COMB_seq2:*
13: /cgn2_6/ptodata/2/pna/US10_NEW_COMB_seq3:*
14: /cgn2_6/ptodata/2/pna/US10_NEW_COMB_seq4:*
15: /cgn2_6/ptodata/2/pna/US11_NEW_COMB_seq5:*
16: /cgn2_6/ptodata/2/pna/US11_NEW_COMB_seq6:*
17: /cgn2_6/ptodata/2/pna/US10_NEW_COMB_seq7:*
18: /cgn2_6/ptodata/2/pna/US11_NEW_COMB_seq8:*
19: /cgn2_6/ptodata/2/pna/US10_NEW_COMB_seq9:*
20: /cgn2_6/ptodata/2/pna/US11_NEW_COMB_seq1:*
21: /cgn2_6/ptodata/2/pna/US11_NEW_COMB_seq2:*
22: /cgn2_6/ptodata/2/pna/US11_NEW_COMB_seq3:*
23: /cgn2_6/ptodata/2/pna/US11_NEW_COMB_seq4:*
24: /cgn2_6/ptodata/2/pna/US11_NEW_COMB_seq5:*
25: /cgn2_6/ptodata/2/pna/US11_NEW_COMB_seq6:*
26: /cgn2_6/ptodata/2/pna/US11_NEW_COMB_seq7:*
27: /cgn2_6/ptodata/2/pna/US10_NEW_COMB_seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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117: /cgn2_6/ptodata/1/pna/us6047_COMB.seq:*

118: /cgn2_6/ptodata/1/pna/us6048_COMB.seq:*

119: /cgn2_6/ptodata/1/pna/us6049_COMB.seq:*

120: /cgn2_6/ptodata/1/pna/us6050_COMB.seq:*

121: /cgn2_6/ptodata/1/pna/us6051_COMB.seq:*

122: /cgn2_6/ptodata/1/pna/us6052_COMB.seq:*

123: /cgn2_6/ptodata/1/pna/us6053_COMB.seq:*

124: /cgn2_6/ptodata/1/pna/us6054_COMB.seq:*

125: /cgn2_6/ptodata/1/pna/us6055_COMB.seq:*

126: /cgn2_6/ptodata/1/pna/us6056_COMB.seq:*

127: /cgn2_6/ptodata/1/pna/us6057_COMB.seq:*

128: /cgn2_6/ptodata/1/pna/us6058_COMB.seq:*

129: /cgn2_6/ptodata/1/pna/us6059_COMB.seq:*

RP

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID

Description

R

```

102: /cgn2_6/ptodata/1/pna/US6032 COMB. seq:*
103: /cgn2_6/ptodata/1/pna/US6034 COMB. seq:*
104: /cgn2_6/ptodata/1/pna/US6035 COMB. seq:*
105: /cgn2_6/ptodata/1/pna/US6036 COMB. seq:*
106: /cgn2_6/ptodata/1/pna/US6037 COMB. seq:*
107: /cgn2_6/ptodata/1/pna/US6038 COMB. seq:*
108: /cgn2_6/ptodata/1/pna/US6039 COMB. seq:*
109: /cgn2_6/ptodata/1/pna/US6040 COMB. seq:*
110: /cgn2_6/ptodata/1/pna/US6041 COMB. seq:*
111: /cgn2_6/ptodata/1/pna/US6042 COMB. seq:*
112: /cgn2_6/ptodata/1/pna/US6043 COMB. seq:*
113: /cgn2_6/ptodata/1/pna/US6044 COMB. seq:*
114: /cgn2_6/ptodata/1/pna/US6045 COMB. seq:*
115: /cgn2_6/ptodata/1/pna/US6046 COMB. seq:*
116: /cgn2_6/ptodata/1/pna/US6047 COMB. seq:*
117: /cgn2_6/ptodata/1/pna/US6048 COMB. seq:*
118: /cgn2_6/ptodata/1/pna/US6049 COMB. seq:*
119: /cgn2_6/ptodata/1/pna/US6050 COMB. seq:*
120: /cgn2_6/ptodata/1/pna/US6051 COMB. seq:*
121: /cgn2_6/ptodata/1/pna/US6052 COMB. seq:*
122: /cgn2_6/ptodata/1/pna/US6053 COMB. seq:*
123: /cgn2_6/ptodata/1/pna/US6054 COMB. seq:*
124: /cgn2_6/ptodata/1/pna/US6055 COMB. seq:*
125: /cgn2_6/ptodata/1/pna/US6056 COMB. seq:*
126: /cgn2_6/ptodata/1/pna/US6057 COMB. seq:*
127: /cgn2_6/ptodata/1/pna/US6058 COMB. seq:*
128: /cgn2_6/ptodata/1/pna/US6059 COMB. seq:*
129: /cgn2_6/ptodata/1/pna/US6059 COMB. seq:*

```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB	ID
------------	-------------	--------------	----	----

Description

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Om protein - nucleic search, using frame_plus_p2n model
 Run on: October 25, 2005, 02:08:13 ; Search time 3255 Seconds
 (without alignments)
 4815.990 Million cel.1 updates/sec

Title: US-10-077-111-13
Perfect score: 2047
Sequence: 1 MVKLIHTIADHGDDVNCCAF.....LTPNRTLKMAINRLETHQK 384

Scoring table: XGAPSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

```
-MODSLI=frame+p2n.model -DBV=xlh
-O=/cgn2_1/usapro_spool/US007711/runat_24102005_072847_8228/app_query.fasta1.583
-DB=PENDING_PARENTS_NA_Main -QMT=Fastap -SUFFX=rnpp -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=hits -START=1 -END=-1 -MATRIX=blipsum62 -TRANS=human40.cdi
-LISP=4 -DOALIGN=200 -THR SCORE=pct -THR MAX=10 -THR MIN=0 -ALIGN=15
-MODA=LOCAL -OUTFMT=PTC -NORM=EXT -HRAPSIZE=500 -MINLEN=2000000000
-USER=US007711 @CGN 1 1 3250 @runat 24102005_072847_8228 -NCPU=6 -ICU=3
-NO MMP -LARGE_PCT -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
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GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 9416466

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Post-processing: Minimum Match 0%
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 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	964.2	75.8	1844	6	AR039277	ORGANISM Homo sapiens (human)
3	912.6	71.7	1254	6	COT29621	REFERENCE AUTHORS Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Juddin, T.B., Casavant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.R., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loguillo, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Iu, X., Gibbs, R.A., Fahey, J., Heitman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Buffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzwicki, M.I., Skalska, U., Smailus, D.E., Schneirach, A., Schein, J.E., Jones, S.J. and Marra, M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
4	893.4	70.2	1919	9	AK129983	PROC. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)
5	890.2	70.0	1811	6	AXT748164	JOURNAL JOURNAL PURNED 12477932 REFERENCE 2 (bases 1 to 1564) AUTHORS Strausberg, R. TITLE Direct Submission JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian Sequence Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
6	890.2	70.0	1811	9	AK093494	
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ALIGMENTS

REMARK	COMMENT
	NIH-MGC Project URL: http://mgc.nci.nih.gov
	Contact: MGC help desk
	Email: cgabba-r@mail.nih.gov
	Tissue Procurement: Miklos Falikovits, M.D., Ph.D.
	CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Yoshiyuki and Piero Carninci (RIKEN)
	DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
	Web site: http://www.shgc.stanford.edu
	Contact: (Dickson, Mark) mcd@paxil.stanford.edu
	R. M.
	clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://Image.Lnl.gov
	This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 22749102.
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Qy	192 TCTCTCTGAGCACAAACATGGCGCTGATAGTGTAGCTTACTGACTGACTGACAT 251
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Qy	252 TCTCTCTGAGCTTCACTCTATGCTGCACTGTGCTGCTGTTCTCCCTTGAGACT 311
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 Reference 1 Schlegel, R., Endege, W.O. and Monahan, J.E.
 Authors Genes differentially expressed in human prostate cancer and their use
 Title Patent: WO 0160860-A 23179 23-AUG-2001;
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Db CQ49179 Definition

Accession CQ49179

Version CQ49179.1 GI:41462815

Keywords

Source Homo sapiens

Organism Homo sapiens (human)